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Roger Proksch and Bruce Moskowitz

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Interactions between single domain particles

Roger Proksch[a)]
School of Physics and Astronomy, University of Minnesota, Minneapolis, Minnesota 55455

Bruce Moskowitz
Department of Geology and Geophysics, Institute for Rock Magnetism, University of Minnesota, Minneapolis, Minnesota 55455

We present a variation of the Wohlfarth–Henkel technique for studying interactions in single domain particles (SDPs) in which samples are prepared in different remanent states before the remanent magnetization curves are measured. By analyzing the resulting series of switching field distributions (SFDs), it is possible to separate the effects of positive (magnetizing) and negative (demagnetizing) interactions, even when one type dominates the other. The method is applied to two types of samples consisting of uniform SPDs of magnetite produced by magnetotactic bacteria: (1) whole bacterial cells containing single, linear chains of SDPs; and (2) SDPs extracted from the cells and allowed to aggregate into clumps.

I. INTRODUCTION

One approach to understanding the effects of interactions in a remanent magnetic system has been a plot of the isothermal remanent magnetization $M_r(H)$ versus the dc-remanent demagnetization $M_d(H)$, where both parameters are normalized to the saturation remanence. These plots, referred to as "Henkel plots,"[1] are based on the work of Wohlfarth[2] who considered the magnetization reversal of a collection of noninteracting uniaxial single domain particles (SDPs). For this case, a Henkel plot is linear, with a slope of -2. When interactions are present, the Henkel plot will be nonlinear and the curvature will depend on whether the interactions are positive (magnetizing) or negative (demagnetizing). In general, a magnetic system can have both positive and negative interactions. Often, however, one type of interaction will be dominant. If a Henkel plot is made of such a system, the dominant interaction may obscure the effects of the other.

In this paper, we present a variation of the Henkel technique for studying interaction effects in which samples are prepared in different remanent states before the remanent magnetization curves are measured. The derivative of each of these remanent curves produces a switching field distribution, ρ_K. By analyzing the resulting series of switching field distributions, it is possible to separate the effects of positive and negative interactions as well as the dependence of the interactions on the remanent state of the system. This technique has been applied to two magnetic systems, each consisting of assemblies of uniform SDPs of magnetite (Fe_3O_4) produced by magnetotactic bacteria.[3] The first system was a collection of whole bacterial cells containing single, linear chains of SDPs. The chains are physically separated from each other by the cell bodies, resulting in a relatively noninteracting sample. The second system was a collection of the same uniform bacterial SDPs extracted from the cells and allowed to agglomerate, resulting in an interacting magnetic system.

[a)]Present address: Department of Physics, Saint Olaf College, Northfield, MN 55057.

II. EXPERIMENTAL METHOD

Samples were first given a saturation remanent magnetization by the application of a large positive field. The $M_d(H)$ curve was then measured to some negative field called the preparation field H_p. At this point, the sample had some net remanent magnetic moment M_p. Starting from this state, $M_r(H)$ was measured. Another large saturating field was again applied, bringing the sample back to its initial state and the process was repeated several times using increasingly larger negative values of H_p. The derivative of $M_r(H)$ with respect to the acquisition field was then ρ_K. All magnetic measurements were made at room temperature with an alternating gradient force magnetometer in fields up to 1000 Oe. The coercivity of the particle samples was always near 300 Oe. Henkel plots were made for comparison with the method outlined above. In this case, the initial state for the $M_r(H)$ curve was produced by dc demagnetization in a negative field equal to the remanent coercivity.

Samples used in this study consisted of a collection of SDPs produced by the magnetotactic bacteria strain MV1.[4] Bacterial SDPs are ideal for interaction studies because of their narrow size and shape distributions. Variations in the coercive fields of bacterial SDPs should be primarily due to interactions rather than a combination of interactions and particle size distribution effects. Magnetotactic bacteria synthesize intracellular membrane bounded magnetite particles called magnetosomes. Magnetosomes in MV1 are truncated hexahedral prisms with average dimensions of $53\times35\times35$ nm.[5] Inside the bacteria, the magnetosomes form a single linear chain of 10–20 particles per cell, with an average distance between magnetosomes of ~10 nm. The magnetosomes are oriented with their magnetic easy axes aligned along the chain axis, forming an effective magnetic dipole. The bacterial dipoles are separated from each other by the cell bodies limiting interchain interaction distances to a few microns. Because of this configuration, negative chain-chain interactions should be small.

Magnetosomes are easily extracted from cells by dissolving the cell membranes in a hypochlorite solution and collecting the magnetic fraction with a magnet. This treatment disrupts the internal chain structure and produces an

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agglomerated sample of SDPs. In such a system, one expects predominantly negative interactions from closed chain configurations.

Samples for remanence measurements were prepared by drying dilute suspensions of whole cells and extracted magnetosomes onto glass slides in the presence of the earth's magnetic field (0.5 Oe). Remanence ratios (M_r/M_s) of ≈0.5, measured from the full hysteresis loops, confirm that samples are randomly oriented and that the drying procedure produced little or no net particle orientation.

III. NONINTERACTING CASE

As a first step in the analysis, we will explore the case of a randomly oriented ensemble of completely noninteracting single domain particles. In this situation, the remanent behavior of the system has been described previously.[6] According to the Stoner–Wohlfarth model of a SDP, the particle coercivity is the same in both the positive and negative directions and depends only on the anisotropy and angle to the applied field. For a random, noninteracting collection of particles, two important points concerning the switching field distribution ρ_K are: The switching field distribution (ρ_K) for remanent acquisition should have a sharp cutoff at the preparation field H_p. Successive ρ_K curves should superpose for fields less than their respective cutoff points. These points are illustrated in Fig. 1(A) for two different preparation fields. Variations from these two ideal conditions indicate the presence of interactions.

IV. INTERACTION CASE

Positive interactions assist the magnetization process, whereas negative interactions hinder it. Therefore, interactions will modify the shape of the ideal noninteracting ρ_K curve in two distinct ways. First, positive interactions will shift ρ_K to lower fields, and for successive initial magnetization states, the ρ_K curves will no longer superpose for fields less than H_p. However, positive interactions should not affect the presence of a sharp cutoff of ρ_K at the preparation field H_p. The positive interaction case is schematically illustrated in Fig. 1(B). Secondly, negative interactions, on the other hand, will shift ρ_K to higher fields. Here, ρ_K curves for successive initial magnetization states will not superpose for fields larger than H_p. This is shown in Fig. 1(C). The more realistic case of both types of interactions is shown in Fig. 1(D).

Thus, the main advantage of our technique over the conventional Henkel plot is that it is possible to observe both positive and negative interactions in a sample with the same measurement. As we will show below, this is true even if one type of interaction dominates.

V. RESULTS

A family of ρ_K curves for an ensemble of whole cells is shown in Fig. 2. As expected, successive curves superimpose for low-field values, indicating minimal positive interactions. Magnetosomes arranged in a chain experience strong magnetic coupling resulting in collective magnetic response. In this case, the positive interactions are so strong that the chain

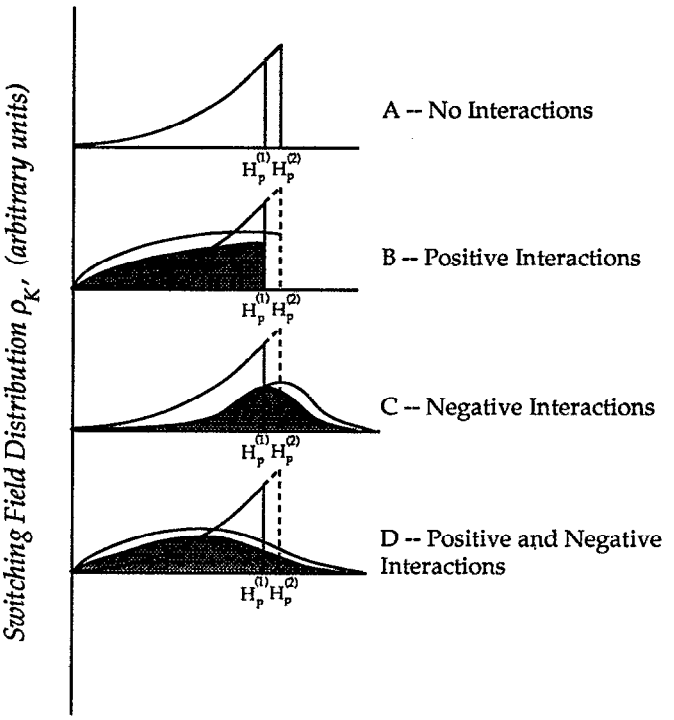

FIG. 1. A set of switching field distribution (ρ_K) curves for single domain particles. Each case [(A)–(D)] provides an example of the behavior of the ρ_K curve for successively increasing preparation field (H_p) values. (A) In the case of no interactions, successive ρ_K curves simply superpose. (B) If there are only positive (magnetizing) interactions present, the system will begin to switch at lower values of $H<H_p$, producing a larger ρ_K at small field values. The system will be completely switched by the time the preparation field is reached, resulting in a cutoff at that point as in the case of no interactions. (C) For the case in which the system exhibits only negative (demagnetizing) interactions, successive curves superpose until the initial preparation field value. Then successive curves will start to diverge as the negative interactions are overcome. To entirely switch the system, it may be necessary to apply a field significantly larger than the preparation field. (D) In the typical situation where both types of interactions are present, features of cases (B) and (C) are combined.

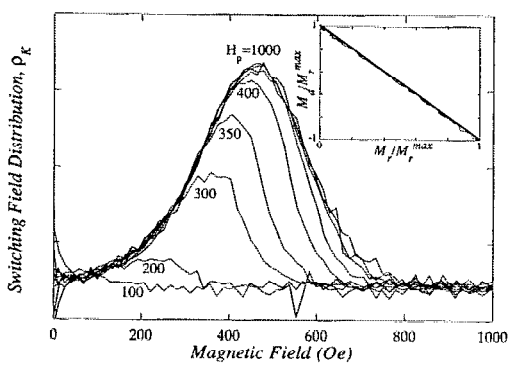

FIG. 2. A family of switching field distribution (ρ_K) curves for relatively noninteracting chains of single domain particles. The numbers on the curves correspond to the preparation field values (H_p). A Henkel plot for the same system is inset in the upper right corner. Whereas the Henkel plot suggests that this is a relatively noninteracting system, the behavior of the ρ_K curves is similar to that diagrammed in Fig. 1(C), indicating the presence of negative interactions.

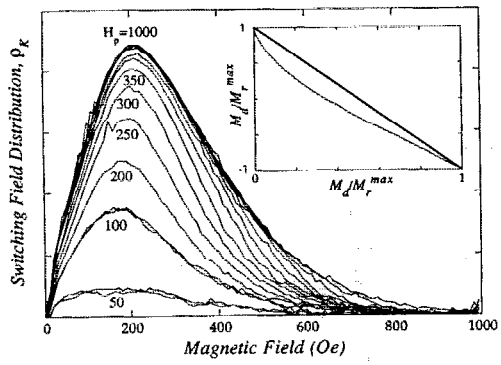

FIG. 3. A family of switching field distribution (ρ_K) curves for a system of highly interacting single domain particles. The numbers on the curves correspond to the preparation field values (H_p). The Henkel plot of this system (shown in the inset in the upper right corner) indicates the presence of negative interactions. This agrees with the family of ρ_K curves. However, the ρ_K curves also indicate the presence of significant positive interactions [see Figs. 1(B) and 1(D)].

of particles behave as a single magnetic particle, which is sufficient enough to maintain the superposition of the ρ_K curves for fields less than H_p. A Henkel plot for this sample (Fig. 2) is approximately linear with slope -2, suggesting no interactions (positive or negative). However, this type of Henkel plot is also similar to theoretical ones produced by aligned chains of particles with a narrow switching field distribution in a 1-D lattice geometry.[7] The ideal 1-D geometry may closely approximate the linear chain microstructure of the whole bacteria cells; however, in our case, the chains are randomly oriented.

Despite a linear Henkel plot for this sample (Fig. 2, inset), the lack of a sharp cutoff at H_p and tailing out at high fields in the ρ_K curves shown in the main part of Fig. 2, indicate the presence of negative interactions. Nevertheless, the shift of successive peaks towards higher fields [see Fig. 1(C)] suggests that the level of negative interactions is small, explaining the linear Henkel plot.

Results for extracted magnetosomes are shown in Fig. 3. Here, successive ρ_K curves do not superimpose, either at low- or high-field values. As expected, the ρ_K curves at high fields show the effects of large negative interactions. For example, a preparation field of 50 Oe requires a field greater than 600 Oe to fully remagnetize the sample (see Fig. 3). A Henkel plot for this sample (Fig. 3) shows the typical response for negative interactions, similar to results from some particulate recording media.[8]

Because this was a random collection of uniform SDPs, some of the particles are expected to interact positively. This is confirmed by nonsuperposition of the ρ_K curves at low fields. Thus, despite the high level of negative interactions, our method was able to pick out a small positive contribution.

VI. CONCLUSIONS

We have demonstrated the utility of examining the switching field distributions of families of remanent curves as a means of separating positive and negative dipolar interactions between single domain particles. In addition, this technique is sensitive to interactions, even when a conventional Henkel plot indicates the system is non-interacting. When interpreting the data shown in this paper, it is important to note that ρ_K depends on both the applied field and the micromagnetic state of the system. In an interacting system, it is possible to have the same bulk magnetization value for very different micromagnetic states. In general, the micromagnetic state is not possible to define, but some statements can be made about it by careful examination of the interactions. Further work is presently in progress in this area.

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